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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/424,840B

DATE: 03/11/2002
 TIME: 09:51:56

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3 <110> APPLICANT: Berchtold, Peter
4   Escher, Robert F. A.
6 <120> TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
8 <130> FILE REFERENCE: 100564-09049
10 <140> CURRENT APPLICATION NUMBER: 09/424,840B
11 <141> CURRENT FILING DATE: 1999-12-03
13 <150> PRIOR APPLICATION NUMBER: DE 19820663.1
14 <151> PRIOR FILING DATE: 1998-05-08
16 <150> PRIOR APPLICATION NUMBER: DE 19755227.7
17 <151> PRIOR FILING DATE: 1997-12-12
19 <150> PRIOR APPLICATION NUMBER: DE 19723904.8
20 <151> PRIOR FILING DATE: 1997-06-06
22 <160> NUMBER OF SEQ ID NOS: 128
24 <170> SOFTWARE: PatentIn version 3.1
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29 <213> ORGANISM: Homo sapiens
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40 1                               5                               10                               15
42 acc ctg tcc ctc aac tgc act gtc tct ggt cgc tcc atc agt ggt tac      96
43 Thr Leu Ser Leu Asn Cys Thr Val Ser Gly Arg Ser Ile Ser Gly Tyr
44                               20                               25                               30
46 tct tgg aga tgg atc cgg cag tct cca ggg aag gga cta gag tgg att      144
47 Ser Trp Arg Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
48                               35                               40                               45
50 ggg gat atc tct tat agt ggg agt acc aag tac aaa ccc tcc ctc agg      192
51 Gly Asp Ile Ser Tyr Ser Gly Ser Thr Lys Tyr Lys Pro Ser Leu Arg
52                               50                               55                               60
54 agt cga gtc acc ctg tca gta gac acg tcc aag aac cag ttc tcc ctg      240
55 Ser Arg Val Thr Leu Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
56 65                               70                               75                               80
58 aag ctg aat tcg gtg acc gct gcg gac acg gcc gtc tat tac tgt gcg      288
59 Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
60                               85                               90                               95
62 cga gtc ttg ccc ttt gac ccg atc tcg atg gac gtc tgg ggc aaa ggg      336
63 Arg Val Leu Pro Phe Asp Pro Ile Ser Met Asp Val Trp Gly Lys Gly

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83          20          25          30
86 Ser Trp Arg Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
87          35          40          45
90 Gly Asp Ile Ser Tyr Ser Gly Ser Thr Lys Tyr Lys Pro Ser Leu Arg
91          50          55          60
94 Ser Arg Val Thr Leu Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
95 65          70          75          80
98 Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
99          85          90          95
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117 <222> LOCATION: (1)..(333)
118 <223> OTHER INFORMATION:
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126 acc atc tct tgt tct ggg agc agc tcc aac atc aga agt aat cct gtt
127 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Arg Ser Asn Pro Val
128          20          25          30
130 agc tgg tat cac cag gtc cca ggc acg gcc ccc aaa ctc ctc atc ttt
131 Ser Trp Tyr His Gln Val Pro Gly Thr Ala Pro Lys Leu Leu Ile Phe
132          35          40          45
134 ggt agt cat cag cgg ccc tca ggg gtc cct gac cga ttc tct ggc tcc
135 Gly Ser His Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
136          50          55          60
138 aag tcg ggc acc tcc gcc tcc ctg gcc atc cgt ggg ctc caa tct ggg
139 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln Ser Gly
140 65          70          75          80

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142 gat gct ggt gac tat tac tgt gca aca tgg gat gac ggc ctc aat ggt      288
143 Asp Ala Gly Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Gly Leu Asn Gly
144              85              90              95
146 ccg gtg ttc ggc gga ggg acc aag ctg acc gtc cta agt cag ccc      333
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163              20              25              30
166 Ser Trp Trp Tyr His Gln Val Pro Gly Thr Ala Pro Lys Leu Leu Ile Phe
167              35              40              45
170 Gly Ser His Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
171              50              55              60
174 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln Ser Gly
175 65              70              75              80
178 Asp Ala Gly Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Gly Leu Asn Gly
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182 Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro
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187 <211> LENGTH: 369
188 <212> TYPE: DNA
189 <213> ORGANISM: Homo sapiens
191 <220> FEATURE:
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193 <222> LOCATION: (1)..(369)
194 <223> OTHER INFORMATION:
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202 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc tat      96
203 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
204              20              25              30
206 gct atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg      144
207 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
208              35              40              45
210 gca gtt ata tca tat gat gga agc aat aaa tac tac gca gac tcc gtg      192
211 Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
212              50              55              60
214 aag ggc cga ttc gcc atc tcc aga gac aat tcc aag aac acg ctg tat      240
215 Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
216 65              70              75              80

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218 ctg caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt      288
219 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
220                               85                      90          95
222 gcg aga gcg ctg ggg agc tgg ggg ggt tgg gac cac tac atg gac gtc      336
223 Ala Arg Ala Leu Gly Ser Trp Gly Gly Trp Asp His Tyr Met Asp Val
224                               100                     105          110
226 tgg ggc aaa ggg acc acg gtc acc gtc tcc tca      369
227 Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
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243                               20                      25          30
246 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
247                               35                      40          45
250 Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
251                               50                      55          60
254 Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
255 65                             70                      75          80
258 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
259                               85                      90          95
262 Ala Arg Ala Leu Gly Ser Trp Gly Gly Trp Asp His Tyr Met Asp Val
263                               100                     105          110
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267                               115                     120
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284 1                               5                      10          15
286 acc atc tct tgt tct gga agc agc tcc aac atc gga agt aat act gta      96
287 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Thr Val
288                               20                      25          30
290 aac tgg tac cag cag ctc cca gga acg gcc ccc aaa ctc ctc atc tat      144
291 Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
292                               35                      40          45
294 agt aat aat cag cgg ccc tca ggg gtc cct gac cga ttc tct ggc tcc      192

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295 Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
296      50                      55                      60
298 aag tct ggc acc tca gcc tcc ctg gcc atc agt ggg ctc cag tct gag      240
299 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu
300 65                      70                      75                      80
302 gat gag gct gat tat tac tgt gca gca tgg gat gac agc ctg aat ggt      288
303 Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly
304      85                      90                      95
306 tgg gtg ttc ggc gga ggg acc aag ctg acc gtc cta ggt cag ccc      333
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326 Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
327      35                      40                      45
330 Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
331      50                      55                      60
334 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu
335 65      70                      75                      80
338 Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly
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353 <222> LOCATION: (1)..(369)
354 <223> OTHER INFORMATION:
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360 1      5                      10                      15
362 tcc ctg aga ctc tct tgt gca gcc tct gga ttt acg ttt gac aac ttt      96
363 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Phe
364      20                      25                      30
366 gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc      144
367 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
368      35                      40                      45
370 tca ggc att agt ggt ggt ggt ctt ttg aca cac tac gca gac tcc gtg      192

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VERIFICATION SUMMARY

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